

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

6. (currently amended) A method of ~~determining a~~ selecting promising candidate nucleotide sequence sequences of an analytical oligo nucleic acid for use in an analysis of a target nucleic acid, the promising candidate nucleotide nucleotide sequences have a high possibility of including a suitable nucleotide sequence of the analytical oligo nucleic acid, the method comprising:

(a) ~~a first calculation step of entering a nucleotide sequence of a target nucleic acid to be analyzed into a computer;~~

(b) calculating an occurrence frequency of each of n unit sequences occurring on ~~a~~ the nucleotide sequence of ~~a~~ the target nucleic acid ~~to be analyzed~~ on the basis of a value of 4^n which ~~correspond~~ corresponds to all of the n unit sequences formed of n nucleotide sequences, wherein n is an integer of 2 or more;

~~(b) a first extraction step of~~ (c) extracting a sequence all candidate sequences having p number of nucleotides and are present on the nucleotide sequence sequences of ~~a~~ the target

nucleic acid, said wherein p is an integer larger than n by m, wherein and m is an integer of 1 or more;

~~(c) a second calculation step of (d) extracting n unit sequences occurring on the contained in each of the candidate sequence sequences; extracted in the first extraction step and obtaining an~~

~~(e) calculating an occurrence frequency index of the candidate sequence sequences on the nucleotide sequence of the target nucleic acid on the basis of the occurrence frequency of each of the n unit sequence calculated in step (b), wherein a lower occurrence frequency index indicates a higher specificity of the candidate sequences to the target nucleic acid; and~~

~~(d) a second extraction step of (f) selecting, a single or a plurality of from the candidate nucleotide sequences extracted in step (c), each of the candidate nucleotide sequences each having a low lower occurrence frequency index based on than a certain threshold value, of the occurrence frequency index obtained from the second calculation step, wherein the lower the occurrence frequency index, the higher the specificity thereby obtaining the promising candidate nucleotide sequences, the certain threshold value being arbitrarily set so that the promising candidate nucleotide sequences are substantially fewer than the candidate nucleotide sequences obtained from step (c)~~

and the suitable nucleotide sequence being included in the
promising candidates.

7. (original) The method according to claim 6, wherein said n
is 5, 6, or 7.

8. (currently amended) The method according to claim 6,
further comprising ~~a third extraction step of selecting, from the~~
promising candidate nucleotide sequences of step (f), a promising
candidate ~~sequence~~ nucleotide sequences having a low stability of
a molecular secondary structure which is not capable of forming a
stable secondary structure, and whereby ~~a sequence~~ more promising
candidate nucleotide sequences which ~~is~~ are capable of readily
hybridizing with ~~a~~ the target nucleic acid under hybridization
conditions ~~is~~ are selected.

9. (previously presented) The method according to claim 8,
wherein the stability of the molecular secondary structure is
determined by at least one property selected from the group
consisting of (i) thermal stability as measured by a value of T_m
and (ii) stability of an intramolecular secondary structure.

10. (currently amended) The method according to claim 9, wherein ~~[[,]] in said third extraction step,~~ a nucleotide sequence having the T_m value falling within a predetermined range is selected from the ~~potential~~ promising candidate nucleotide sequences and ~~forming~~ which forms an unstable secondary structure is further selected.

11. (currently amended) The method according to any one of claims 6 to 10, wherein all of the calculations involved in steps (a) to ~~(d)~~ (f) are sequentially performed by a computer.

12. (previously presented) The method according to any one of claims 6 to 10, wherein said nucleotide sequence of an analytical oligo nucleic acid is used in (i) a PCR method for detecting a specific nucleotide sequence present in a nucleotide sequence of a nucleic acid by using an enzyme reaction which requires hybridization reactions of a nucleic acid, or (ii) in a hybridization reaction of a nucleic acid employing a probe.